



```

DB 905 LPTCAVCLERMDS--VLAICNHSFHARCLQWAD-----NTPCVR 945

RESULT 2
ID Y057_CAEEL STANDARD: PRT: 235 AA.
AC 009463;
DR 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 24.9 kDa protein Cl6C10.7 in chromosome III.
GN Cl6C10.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Lloyd C.;
RL Submitted (NOV-1994) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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DR EMBL: 246787; CAAB6745.1; -
DR Wormpep: C16C10.7; ZNF1498.
DR InterPro: IPR000306; Znf_FYVE.
DR InterPro: IPR001841; Znf_Fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00064; FYVE; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Hypothetical protein ZINC-finger.
KM ZN_FING 26 67 RING-TYPE.
FT ZN_FING 121 124 POLY-GLY.
FT DOMAIN 169 172 POLY-ALA.
SQ SEQUENCE 235 AA; 24915 MW; 21A04AE951F6382A CRC64;

Query Match 33.1%; Score 97; DB 1; Length 235;
Best Local Similarity 40.0%; Pred. No. 3.7e-05;
Matches 18; Conservative 6; Mismatches 17; Indels 4; Gaps 2;

OY 4 CTCSDFFDHSRDVAIHCGHPEHLOCLQWETAP-SRTCPQCR 47
DB 26 CNIC---LDAKDAVVSILCGHLCFPCQLSQWLDTRNNQVCPVK 67

RESULT 3
ID MKR3_MOUSE STANDARD: PRT: 544 AA.
AC 060764;
DR 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Makorin 3 (Zinc-finger protein 127).
GN MKR3 OR ZFP127 OR ZNF127.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX Pubmed=10196368;
RA Jong M.T.C., Carey A.H., Caldwell K.A., Lau M.H., Handel M.A.,

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RA Driscoll D.J., Stewart C.L., Rinchik E.M., Nicholls R.D.;
RT "Imprinting of a RING zinc-finger encoding gene in the mouse
RT chromosome region homologous to the Prader-Willi syndrome genetic
RT region.";
RM Hum. Mol. Genet. 8:795-803(1999).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 3 C3H1-TYPE ZINC FINGERS.
-----
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-----
DR EMBL: U19106; AAA76863.1; -
DR MGD: MGI:99138; Zfp127.
DR InterPro: IPR000571; Zf-CCCH.
DR InterPro: IPR001841; Znf_Fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00642; zf-CCCH; 3.
DR SMART: SM00184; RING; 1.
DR SMART: SM00356; Znf_C3H1; 3.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KM Zinc-finger: Repeat.
FT ZN_FING 98 116 C3H1-TYPE 1.
FT ZN_FING 280 298 C3H1-TYPE 2.
FT DOMAIN 302 329 MAKORIN-TYPE CVS-HIS.
FT ZN_FING 347 401 RING-TYPE.
FT ZN_FING 436 456 C3H1-TYPE 3.
SQ SEQUENCE 544 AA; 59444 MW; FF05B7D034C5EA9F CRC64;

Query Match 32.6%; Score 95.5; DB 1; Length 544;
Best Local Similarity 31.7%; Pred. No. 0.00013;
Matches 19; Conservative 9; Mismatches 21; Indels 11; Gaps 2;

OY 3 LCTICSDFFDHSRDA-----AHCGHPEHLOCLQW-----FETAPSRTPQCRIOYG 51
DB 346 VCGICMEVVEYKADPTDRRGILFSCNHYCYLCKIRRMWSATQFENRISKSCPCRVSSG 405

RESULT 4
ID GOL1_DROME STANDARD: PRT: 284 AA.
AC 006003;
DR 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Goliah protein (G1 proteio).
GN GOL OR G1 OR GL.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Eukaryota; Metazoa; Insecta; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA MEDLINE=93216124; Pubmed=8462875;
RA Bouchard M.L., Core S.;
RT "The Drosophila melanogaster developmental gene g1 encodes a variant
RT zinc-finger motif protein.";
RL Gene 125:205-209(1993).
CC -1- FUNCTION: REGULATION OF GENE EXPRESSION DURING MESODERM FORMATION.
CC -1- PUTATIVE ROLE AS TRANSCRIPTION FACTOR.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: VISCERAL MESODERM AND PRIMORDIA OF SOMATIC
CC MUSCULATURE.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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DR EMBL; J01495; J01495.  
 DR PIR; M97204; AAA28582.1; -  
 DR PIR; J01495; J01495.  
 DR FlyBase; FBgn0004919; gol.  
 DR InterPro; IPR001841; ZnF\_fing.  
 DR Pfam; PF00097; zf-C3HC4; 1.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
 DR PROSITE; PS50089; ZF\_RING\_2; 1.  
 DR Developmental protein; Zinc-finger; Transcription regulation;  
 KW DNA-binding; Nuclear protein.  
 FT ZN\_FING 126 167 RING-TYPE.  
 FT DOMAIN 208 259 GLN/PRO/SER-RICH.  
 SQ SEQUENCE 284 AA; 31973 MW; ECE2D5EDBA1E2B CRC64;

Query Match 31.4%; Score 92; DB 1; Length 284;  
 Best Local Similarity 31.9%; Pred. No. 0.00019;  
 Matches 15; Conservative 8; Mismatches 22; Indels 2; Gaps 1;

QY 4 CTCTGDFDHSRDVAIHCGHTFHLOCLQWETAPSTRCTPCQCR 50  
 Db 126 CALCIENAVKPTDTRILPCKEHFKNCIDPWL--IEHRTCPMKLDV 170

RESULT 5  
 TTCC3\_HUMAN STANDARD; PRT; 2025 AA.

AC P53804; P78476; P78477;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tetrairicopeptide repeat protein 3 (TPR repeat protein D).  
 GN TTCC3 OR TPRD.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=96281123; PubMed=8724848;  
 RA Ohira M., Ootsuyama A., Suzuki E., Ichikawa H., Seki N.,  
 RA Nagase T., Nomura N., Ohki M.;  
 RT "Identification of a novel human gene containing the  
 RT tetrairicopeptide repeat domain from the Down syndrome region of  
 RT chromosome 21.";  
 RL DNA Res. 3:9-16(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Petal brain;  
 RX MEDLINE=97103476; PubMed=8947847;  
 RA Tsukahara F., Hattori M., Muraki T., Sakaki Y.;  
 RT "Identification and cloning of a novel cDNA belonging to  
 RT tetrairicopeptide repeat gene family from Down syndrome-critical  
 RT region 21q22.2.";  
 RL J. Biochem. 120:820-827(1996).  
 RN [3]  
 RP ALTERNATIVE PRODUCTS: 3 ISOFORMS: TPDI (SHOWN HERE), TPDI1  
 AND TPDI11; SEEMS TO BE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: FOUND IN ALL TISSUES EXAMINED.  
 CC -1- SIMILARITY: CONTAINS 4 TPR REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
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DR EMBL; D83077; BAA11769.1; -  
 DR EMBL; D84294; BAA12301.1; -  
 DR EMBL; D84295; BAA12302.1; -  
 DR EMBL; D84296; BAA12303.1; -  
 DR MIM; 602259; -  
 DR InterPro; IPR001440; TPR.  
 DR InterPro; IPR001841; ZnF\_fing.  
 DR Pfam; PF00097; TPR; 4.  
 DR Pfam; PF00097; zf-C3HC4; 1.  
 DR SMART; SM00184; RING; 1.  
 DR SMART; SM00028; TPR; 3.  
 DR PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
 DR PROSITE; PS50089; ZF\_RING\_2; 1.  
 KW Repeat; TPR repeat; Zinc-finger; Alternative splicing.  
 FT REPEAT 231 264 TPR 1.  
 FT REPEAT 266 298 TPR 2.  
 FT REPEAT 536 572 TPR 3.  
 FT REPEAT 576 609 TPR 4.  
 FT ZN\_FING 1957 1997 RING-TYPE.  
 FT DOMAIN 453 456 POLY-SER.  
 FT DOMAIN 1020 1029 POLY-LYS.  
 FT DOMAIN 1899 1902 POLY-LYS.  
 FT DOMAIN 1018 1029 ARG/LYS-RICH (BASIC).  
 FT DOMAIN 1172 1185 ARG/LYS-RICH (BASIC).  
 FT DOMAIN 1563 1579 ARG/LYS-RICH (BASIC).  
 FT VARSPLIC 1 233 MISSING (IN ISOFORM TPDI11).  
 FT VARSPLIC 1 310 MISSING (IN ISOFORM TPDI11).  
 SQ SEQUENCE 2025 AA; 229889 MW; 1B4BCAA3684B6253 CRC64;

Query Match 31.2%; Score 91.5; DB 1; Length 2025;  
 Best Local Similarity 37.0%; Pred. No. 0.0014;  
 Matches 17; Conservative 7; Mismatches 19; Indels 3; Gaps 2;

QY 2 SLCTGDFDHSRDVAIHCGHTFHLOCLQWETAPSTRCTPCQCR 47  
 Db 1955 SSGEICHEVF-KSRNVAVLKCGHKYHKGCFKQWLK--GGSACPACQ 1997

RESULT 6  
 MKR4\_HUMAN STANDARD; PRT; 485 AA.

AC Q13434;  
 DT 01-MAR-2002 (Rel. 41, Created)  
 DT 01-MAR-2002 (Rel. 41, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Makorin 4 (Zinc-finger protein 127-Xp) (ZNF127-Xp).  
 GN MKR4 OR ZNF127L1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hendrich B.D., Longstreet M., Gustashaw K., Nicholls R.D.,  
 RA Willard H.F.;  
 RT "An X-linked homologue of the autosomal imprinted gene ZNF127  
 RT escapes X chromosome inactivation.";  
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 CC -1- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.  
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 -----  
 CC EMBL: U41315; AAA99070.1; -.  
 DR InterPro: IPR000571; Zf-CCCH.  
 DR InterPro: IPR001841; Znf\_fing.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR Pfam: PF00642; zf-CCCH; 4.  
 DR SMART: SM00184; RING; 1.  
 DR SMART: SM00356; znf-C3H1; 4.  
 DR PROSITE: PS00518; ZF\_RING\_1; 1.  
 DR PROSITE: PS50089; ZF\_RING\_2; 1.  
 DR Zinc-finger; Repeat.  
 FT ZN\_FING 96 114 C3H1-TYPE 1.  
 FT ZN\_FING 125 143 C3H1-TYPE 2.  
 FT ZN\_FING 249 267 C3H1-TYPE 3.  
 FT DOMAIN 271 298 MAKORIN-TYPE CYS-HIS.  
 FT ZN\_FING 316 370 RING-TYPE.  
 FT ZN\_FING 405 425 C3H1-TYPE 4.  
 SQ SEQUENCE 485 AA; 52909 MW; AE28B962544CEFFE CRC64;

Query Match 30.9%; Score 90.5; DB 1; Length 485;  
 Best Local Similarity 32.8%; Pred. No. 0.00047;  
 Matches 19; Conservative 12; Mismatches 14; Indels 13; Gaps 3;

OY 3 LCTICSDFF-----DHSRDVAIHCGHPTHLOCLIQW-----FETAPSRTPCQCR 48  
 Db 315 VCGICMEVYVYKANKPNNEHREILIS-NCNHTPTCLCKIRKRSKAFESRIYKSCPCQCR 371

RESULT 7  
 YHBO\_YEAST  
 ID YHBO\_YEAST STANDARD; PRT; 585 AA.  
 AC P38748;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical 67.5 kDa protein in PRPS4-STRE20 intergenic region.  
 GN YH010C.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 ON NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C / AB972;  
 RX MEDLINE=94378003; PubMed=8091229;  
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,  
 Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,  
 R. Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,  
 R. Latreille P., Louis E.J., Macri C., Mardis E., Meneses S., Mouser L.,  
 Nham M., Rifkin L., Riles L., St. Peter H., Trevaskis E., Vaughan K.,  
 Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,  
 Vaubin M.;  
 RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome  
 VIII."  
 RL Science 265:2077-2082(1994).  
 CC -!- SIMILARITY: TO C.ELEGANS EED8.9 AND S.POMBE SPAC16P8.13.  
 CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
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 CC -----  
 CC EMBL: U11582; CAB34905.1; -.  
 DR PIR: S46825; S46825.  
 DR SGD: S0001002; YH010C.  
 DR InterPro: IPR001841; Znf\_fing.  
 DR InterPro: IPR001607; zf-UBP.  
 X

DR Pfam: PF00097; zf-C3HC4; 1.  
 DR Pfam: PF02148; zf-UBP; 1.  
 DR SMART: SM00184; RING; 1.  
 DR SMART: SM00290; Znf\_UBP; 1.  
 DR PROSITE: PS00518; ZF\_RING\_1; FALSE-NEG.  
 DR PROSITE: PS50089; ZF\_RING\_2; 1.  
 KW Hypothetical protein; Zinc-finger.  
 FT ZN\_FING 240 280 RING-TYPE.  
 SQ SEQUENCE 585 AA; 67503 MW; 88FF670CC73A1263 CRC64;

Query Match 30.9%; Score 90.5; DB 1; Length 585;  
 Best Local Similarity 37.5%; Pred. No. 0.00056;  
 Matches 18; Conservative 6; Mismatches 19; Indels 5; Gaps 2;

OY 1 LSLCTICSDFFD-HSRDVAIHCGHPTHLOCLIQWFEETAPSRTPCQCR 47  
 Db 237 LPTCPVCLERMDSETGLVTIPCOHPTHCCCLNKM-----KNSRCPVCR 280

RESULT 8  
 YQUD\_CAEEL  
 ID YQUD\_CAEEL STANDARD; PRT; 161 AA.  
 AC P30631;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical 18.8 kDa protein ZK637.14 in chromosome III.  
 GN ZK637.14.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;  
 OC Rhabditidae; Peloderiinae; Caenorhabditis.  
 ON NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RX MEDLINE=92168156; PubMed=1538779;  
 RA Sulston J., Du Z., Thomas K., Wilson R., Hillier L., Staden R.,  
 R. Halloran N., Green P., Thierry-Mieg J., Olu L., Dear S., Coulson A.,  
 R. Craxton M., Durbin R.K., Berts M., Metzstein M., Hawkins T.,  
 R. Ainscough R., Waterston R.;  
 RT "The C. elegans genome sequencing project: a beginning."  
 RL Nature 356:37-41(1992).  
 CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 CC -----

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 CC -----  
 CC EMBL: Z11115; CAA77447.1; -.  
 DR PIR: S15788; S15788.  
 DR WormPep: ZK637.14; CE00432.  
 DR InterPro: IPR001841; Znf\_fing.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS00518; ZF\_RING\_1; FALSE-NEG.  
 DR PROSITE: PS50089; ZF\_RING\_2; 1.  
 KW Hypothetical protein; Zinc-finger.  
 FT ZN\_FING 72 134 RING-TYPE.  
 SQ SEQUENCE 161 AA; 18847 MW; F5EF9F3A83A9C027 CRC64;

Query Match 30.5%; Score 89.5; DB 1; Length 161;  
 Best Local Similarity 29.4%; Pred. No. 0.00022;  
 Matches 20; Conservative 5; Mismatches 20; Indels 23; Gaps 2;

OY 4 CTICSDFFDHSRDVAIHH-----CGHPTHLOCLIQWFEETAPSRTP 42  
 Db 72 CALCLDMLQNNVDIPEDHVIKEELKIDPTFTGTVIVMPCKHREHFCPLTLMLEA--QQT 129



Db 350 LCKICA---ESNKKYKIEPCGHLSCCLAM-CHSDSOTPCRCCEI 393

RESULT 11

ID RN12\_HUMAN STANDARD; PRT; 624 AA.

AC Q9NWV2; Q9Y598;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE RING finger protein 12 (LIM domain interacting RING finger protein)

DE (RING finger LIM domain-binding protein) (R-LIM) (NY-REN-43 antigen).

GN RNF12 OR RLIM.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20469411; PubMed=11013082;

RA Ostendorf H.P., Bossenz M., Mincheva A., Copeland N.G., Gilbert D.J., Jenkins N.A., Lichter P., Bach I.

RT "Functional characterization of the gene encoding RLIM, the corepressor of LIM homeodomain transcription factors.";

RL Genomics 69:120-130(2000).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=99438124; PubMed=10508479;

RA Scanlan M.J., Gordon J.D., Williamson B., Stockert E., Bander N.H., Jongsma V., Gure A.O., Jager D., Jager E., Knuth A., Chen Y.-T., Old L.J.

RT "Antigens recognized by autologous antibody in patients with renal-cell carcinoma.";

RL Int. J. Cancer 83:456-464(1999).

RN [3]

RP SEQUENCE FROM N.A.

RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Magatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuno Y., Niimura K., Watanabe T.

RT "NEDO human cDNA sequencing project.";

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: ACTS AS A NEGATIVE CO-REGULATOR FOR LIM HOMEODOMAIN TRANSCRIPTION FACTORS. VIA THE RECRUITMENT OF THE SIN3A/HISTONE DEACETYLASE COREPRESSOR COMPLEX.

CC -1- SUBUNIT: ASSOCIATES WITH LIM/HOMEOBOX FACTORS.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY TISSUES.

CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

CC -1- CAUTION: REF.2 DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS IN POSITION 134 AND 142.

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CC -----

CC EMBL: AJ271670; CAC14228.1; -

DR EMBL: AF155109; AAD42875.1; ALT\_FRAME.

DR EMBL: AK001334; BAA91632.1; -

DR InterPro: IPR003837; Glu-TRNAGln.

DR InterPro: IPR002190; PHD.

DR InterPro: IPR001965; MAG.

DR InterPro: IPR001841; Znf\_ring.

DR Pfam: PF02686; Glu-TRNAGln; 1.

DR Pfam: PF01454; MAG; 1.

DR Pfam: PF00628; PHD; 1.

DR Pfam: PF00097; Zf-C3HC4; 1.

DR SMART: SM00184; RING; 1.

DR PROSITE: PS00518; ZF\_RING\_1; FALSE\_NEG.

DR PROSITE: PS50089; ZF\_RING\_2; 1.

KW Transcription regulation; Zinc-finger.

FT DOMAIN 422 506

FT ZN\_FING 570 611

FT DOMAIN 453 481

FT DOMAIN 500 506

FT CONFLICT 126 126

FT CONFLICT 134 134

FT CONFLICT 144 145

FT CONFLICT 418 418

SQ SEQUENCE 624 AA; 68527 MW; DE3ADE09ACACBCF8 CRC64;

Query Match 30.0%; Score 88; DB 1; Length 624;

Best Local Similarity 27.7%; Pred. No. 0.0012;

Matches 13; Conservative 11; Mismatches 21; Indels 2; Gaps 1;

Oy 1 LSCTICDFDHSRDVAIHCGHTPHLOCTIOMFERAPSRTPQCR 47

Db 567 LKTCVCITTEYEGNKLRLPCSHETHVHCIDRWL--SENSTPCR 611

RESULT 12

ID Y055\_CAEEL STANDARD; PRT; 409 AA.

AC Q09251;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical 47.6 kDa protein Cl6C10.5 in chromosome III.

GN Cl6C10.5

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI\_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC SRRAN-BRISTOL N2;

RA Lloyd C.

RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

CC -----

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CC -----

CC EMBL: Z46787; CAA86743.1; -

DR WormPep: Cl6C10.5; CE01496.

DR InterPro: IPR001841; Znf\_ring.

DR Pfam: PF00097; Zf-C3HC4; 1.

DR SMART: SM00184; RING; 1.

DR PROSITE: PS00518; ZF\_RING\_1; FALSE\_NEG.

DR PROSITE: PS50089; ZF\_RING\_2; 1.

KW Hypothetical protein; Transmembrane; Zinc-finger.

FT ZN\_FING 296 358

FT TRANSMEM 122 142

FT TRANSMEM 147 167

FT TRANSMEM 174 194

FT TRANSMEM 218 238

FT TRANSMEM 243 263

FT TRANSMEM 388 408

SQ SEQUENCE 409 AA; 47627 MW; 6AB33FC9D026C461 CRC64;

Query Match 29.9%; Score 87.5; DB 1; Length 409;

Best Local Similarity 26.9%; Pred. No. 0.00095;



```
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC or send an email to license@lsb-sib.ch).
CC -----
DR EMBL: M64067; AAA37299.1; -.
DR EMBL: M64068; AAA37301.1; ALT_SEQ.
DR EMBL: M64279; AAA37300.1; -.
DR PIR: A39523; A39523.
DR PIR: A39524; A39524.
DR MGD: MGI:88174; Bm11.
DR InterPro: IPR001841; Znf_Ring.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Chromatin regulator: Nuclear protein: Transcription regulation;
DR Repressor: Zinc-finger: Proto-oncogene.
FT ZN_FING 18 57 RING-TYPE.
FT DOMAIN 81 95 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 249 324 PRO/SER-RICH.
SQ SEQUENCE 324 AA; 36707 MW; AD7DECDB6B29DC55 CRC64;

Query Match 29.7%; Score 87; DB 1; Length 324;
Best Local Similarity 33.3%; Pred. No. 0.00088;
Matches 16; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

QY 3 LCTICSDPFDSRDVAAIHGCHFHLOCLIQWTFAPSRCPQCRIOV 50
Db 17 MCVLCGGYFIDATYI--TECLHSFCKTCIVRYLET--SKYCPIDVOY 60

RESULT 15
BMIT_HUMAN STANDARD; PRT; 326 AA.
AC P35226; Q96F37;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Polcomb complex protein BMT-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Erythrocyte;
RX MEDLINE=94093545; PubMed=8268912;
RA Alkema M.J., Wiegand J., Raap A.K., Berns A., van Lohuizen M.;
RT "Characterization and chromosomal localization of the human proto-
RT oncogene BMT-1.";
RL Hum. Mol. Genet. 2:1597-1603(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN MAINTAINING THE TRANSCRIPTIONALLY REPRESSIVE
CC STATE OF GENES. MODIFIES CHROMATIN, RENDERING IT HERITABLY CHANGED
CC IN ITS EXPRESSIBILITY.
CC -1- SUBUNIT: COMPONENT OF THE CHROMATIN-ASSOCIATED POLYCOMB COMPLEX
CC (PCG).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DISEASE: COOPERATES WITH THE MCG ONCOGENE TO PRODUCE B LYMPHOMAS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
```

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CC or send an email to license@lsb-sib.ch).
CC -----
DR EMBL: L13689; AAA19873.1; -.
DR EMBL: BC011652; AAH11652.1; -.
DR MIM: 164831; -.
DR InterPro: IPR001841; Znf_Ring.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Chromatin regulator: Nuclear protein: Transcription regulation;
DR Repressor: Zinc-finger: Proto-oncogene.
FT ZN_FING 18 57 RING-TYPE.
FT DOMAIN 81 95 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 251 326 PRO/SER-RICH.
FT CONFLICT 265 265 V>I (IN REF. 2).
SQ SEQUENCE 326 AA; 36935 MW; 118BED396B2BA43 CRC64;

Query Match 29.7%; Score 87; DB 1; Length 326;
Best Local Similarity 33.3%; Pred. No. 0.00088;
Matches 16; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

QY 3 LCTICSDPFDSRDVAAIHGCHFHLOCLIQWTFAPSRCPQCRIOV 50
Db 17 MCVLCGGYFIDATYI--TECLHSFCKTCIVRYLET--SKYCPIDVOY 60

RESULT 16
2147_MOUSE STANDARD; PRT; 634 AA.
AC O61510;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Zinc finger protein 147 (Estrogen responsive finger protein) (Efp).
GN ZNF147 OR ZFP147 OR EFP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus, Ovary, and Placenta;
RX MEDLINE=96025835; PubMed=7592654;
RA Orino A., Inoue S., Ikeda K., Noji S., Muramatsu M.;
RT "Molecular cloning, structure, and expression of mouse estrogen-
RT responsive finger protein Efp. Co-localization with estrogen receptor
RT mRNA in target organs.";
RL J. Biol. Chem. 270:24406-24413(1995).
CC -1- FUNCTION: MEDIATES ESTROGEN ACTION IN VARIOUS TARGET ORGANS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 1 SPRY DOMAIN.
CC -----
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CC -----
DR EMBL: D63902; BA09941.1; -.
DR MGD: MGI:102749; Zfp147.
DR InterPro: IPR001870; Gamma_carboxylase.
DR InterPro: IPR003877; SPRY.
DR InterPro: IPR003878; SPRY_domain.
```



[illegible]

DR EMBL; AF277164; AAC27595.1; JOINED.  
DR EMBL; AF277165; AAG27595.1; JOINED.  
DR EMBL; AF277166; AAG27595.1; JOINED.  
DR EMBL; AF277167; AAG27595.1; JOINED.  
DR EMBL; AF277168; AAG27595.1; JOINED.  
DR EMBL; AF277169; AAG27595.1; JOINED.  
DR EMBL; AF161555; AAF29042.2; -.  
DR EMBL; BC001799; AAH01799.1; -.  
DR InterPro: IPR000571; Zf-CCCH.  
DR InterPro: IPR001841; ZnF\_fing.  
DR Pfam: PF00097; Zf-CCHC4; 1.  
DR Pfam: PF00642; Zf-CCCH; 4.  
DR SMART; SM00184; RING; 1.  
DR SMART; SM00356; znf\_C3H1; 4.  
DR PROSITE: PS00518; ZF\_RING\_1; 1.  
DR PROSITE: PSS0089; ZF\_RING\_2; 1.  
KW Zinc-finger; Repeat.  
FT ZN\_FING 8 C3H1-TYPE 1.  
FT ZN\_FING 37 55 C3H1-TYPE 2.  
FT ZN\_FING 171 189 C3H1-TYPE 3.  
FT DOMAIN 193 222 MAKORIN-TYPE CYS-HIS.  
FT ZN\_FING 238 292 MAKORIN-TYPE  
FT ZN\_FING 327 347 RING-TYPE.  
FT CONFLICT 186 186 C3H1-TYPE 4.  
FT CONFLICT 186 186 F -> V (IN REF. 2 AND 3).  
FT CONFLICT 278 278 K -> E (IN REF. 2).  
SQ SEQUENCE 416 AA; 46988 MW; 02B6B7A8BD382DDC CRC64;

Query Match 29.5%; Score 86.5; DB 1; Length 416;  
Best Local Similarity 29.8%; Pred. No. 0.0013;  
Matches 17; Conservative 10; Mismatches 19; Indels 11; Gaps 2.

3 LCTTCSDF-----DHSRDVAIHCGHFPHLOCLIQW----FEFASTRPCQCR 48  
::|||: | ::|||: |||: |||: |||: |||: |||: |||: |||: |||:  
Db 237 VCSTICMEVILEKASASERRFGILSCNTFYLCISCIROMRCAKQGFNPITKSPEECRV 293

RESULT 18  
MKR2\_MOUSE STANDARD: PRT; 416 AA.  
AC OPERVL: Q9DOL9;  
DT 01-MAR-2002 (Rel. 41, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Makorin 2.  
GN MKRN2.  
OS Mus musculus (Mouse).  
OC Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Embryota; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21481893; PubMed=11597136;  
RA Gray T.A., Azama K., Whitmore K., Min A., Abe S., Nicholls R.D.;  
RT "Phylogenetic conservation of the makorin-2 gene, encoding a multiple  
TL zinc-finger protein, antisense to the raf1 proto-oncogene".  
RL Genomics 77:119-126(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Embryo;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shnagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Itawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,  
RA Kuohji P., Lewis S., Matsuo Y., Nikaido I., Plesio G., Quackenbush J.,  
RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Oikido T., Furuno M., Aono H., Baldarelli R., Barish G.,  
RA Blake J., Botfield D., Boujunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Butl C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
RA Wyszewski A., Yoshida K., Hasegawa Y., Kawaji H., Kontsuki S.,  
RA Hayashizaki Y.,  
RT "Functional annotation of a full-length mouse cDNA collection";  
RL Nature 409:685-690(2001).  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
CC -1- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.  
CC -----  
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CC -----  
DR EMBL: AF277171; MAG27596.1; -  
DR EMBL: AK011295; BAB27523.1; -  
DR MGI: 1914277; Mkr2.  
DR InterPro: IPR000571; Zf-CCCH.  
DR InterPro: IPR001841; Znf-Fing.  
DR Pfam: PF00097; Zf-C3HC4; 1.  
DR Pfam: PF00642; Zf-CCCH; 4.  
DR SMART: SM00184; RING; 1.  
DR SMART: SM00356; Znf-C3H1; 4.  
DR PROSITE: PS00518; ZF\_RING\_1; 1.  
DR PROSITE: PS50089; ZF\_RING\_2; 1.  
DR Zinc-finger; Repeat.  
KM ZN\_FING 8 C3H1-TYPE 1.  
FT ZN\_FING 37 55 C3H1-TYPE 2.  
FT ZN\_FING 171 189 C3H1-TYPE 3.  
FT DOMAIN 193 222 MAKORIN-TYPE CYS-HIS.  
FT ZN\_FING 238 292 RING-TYPE.  
FT ZN\_FING 327 347 C3H1-TYPE 4.  
FT CONFLICT 181 181 L -> F (IN REF. 2).  
SQ SEQUENCE 416 AA; 46562 MW; 5F268EB9D9A6C9F CRC64;  
  
Query Match 29.5%; Score 86.5; DB 1; Length 416;  
Best Local Similarity 29.8%; Pred. No. 0.0013;  
Matches 17; Conservative 10; Mismatches 19; Indels 11; Gaps 2;  
  
QY 3 LCCTCSDFP-----DHSRDVAIHGCHTFHLOCLIOW-----RPTASRRCPCORI 48  
Db 237 VCSICMEVILEKASASERRRGIISNCSTHTYCLSCIRWRCRCAKOPENPTINSCEPCRV 293  
  
RESULT 19  
YDRD\_SCHPO STANDARD; PRT; 547 AA.  
ID YDRD\_SCHPO  
AC 013747;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical 61.8 kDa protein Cl6E8.13 in chromosome I.  
GN SPAC16E8.13.  
OS Schizosaccharomyces pombe (fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
ON NCBI\_Taxid=4896;  
RX [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=912;  
RA Oliver K., Harris D., Barrell B.G., Rajandream M.A., Wood V.;  
RL Submitted (JUG-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: TO YEAST YHLO10C AND C.ELEGANS REED8.9.  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
CC -----  
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CC -----  
DR EMBL: Z98529; CAB11041.1; -  
DR InterPro: IPR001841; Znf\_Fing.  
DR InterPro: IPR001607; Zf-UBP.  
DR Pfam: PF00097; Zf-C3HC4; 1.  
DR Pfam: PF02148; Zf-UBP; 1.  
DR SMART: SM00184; RING; 1.  
DR SMART: SM00290; Znf-UBP; 1.  
DR PROSITE: PS00518; ZF\_RING\_1; FALSE\_NEG.  
DR PROSITE: PS50089; ZF\_RING\_2; 1.  
KM Hypothetical protein; Zinc-finger.  
FT ZN\_FING 208 248 RING-TYPE.  
FT DOMAIN 526 534 POLY-LYS.  
SQ SEQUENCE 547 AA; 61825 MW; 2C3FDB4FD7CF70E1 CRC64;  
  
Query Match 29.5%; Score 86.5; DB 1; Length 547;  
Best Local Similarity 37.5%; Pred. No. 0.0017;  
Matches 18; Conservative 6; Mismatches 19; Indels 5; Gaps 2;  
  
QY 1 LSLCTCSDFPDS-RVVAIHGCHTFHLOCLIOFWFTASRRCPCORI 47  
Db 205 LPTCVCLERMDSITRGLITIVCOHTFHCPLQW----GNSSCPVCR 248  
  
RESULT 20  
MEL1\_MOUSE STANDARD; PRT; 342 AA.  
ID MEL1\_MOUSE  
AC P23798;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE DNA-binding protein Mel-18.  
GN ZNF144 OR ZFP144 OR ZFP-144 OR MEL18 OR MEL-18.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
ON NCBI\_Taxid=10090;  
RX [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91060627; PubMed=2246278;  
RA Tagawa M., Sakamoto T., Shigemoto K., Matsubara H., Tamura Y.,  
RA Ito T., Nakamura I., Okitsu A., Imai K., Taniguchi M.;  
RT "Expression of novel DNA-binding protein with zinc finger structure  
RT in various tumor cells";  
RL J. Biol. Chem. 265:20021-20026(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP CHARACTERIZATION.  
RX MEDLINE=96091139; PubMed=8521824;  
RA Kanno M., Hasegawa M., Ishida A., Isono K., Taniguchi M.;  
RT "mel-18, a Polycomb group-related mammalian gene, encodes a  
RT transcriptional negative regulator with tumor suppressive activity";  
RL EMBO J. 14:5672-5678(1995).  
CC -1- FUNCTION: TRANSCRIPTIONAL REPRESSOR. BINDS SPECIFICALLY TO THE  
CC DNA SEQUENCE 5'GACTGACT-3'. HAS A TUMOR SUPPRESSOR ACTIVITY.  
CC MAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEURAL  
CC CELL DEVELOPMENT.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TUMOR CELLS AND  
CC IN NEURAL TISSUES.  
CC -1- DEVELOPMENTAL STAGE: DEVELOPMENTALLY REGULATED.  
CC -1- DISEASE: PROBABLY RELATED TO TUMORGENESIS SINCE IT IS EXPRESSED  
CC STRONGLY IN MOST TUMOR CELL LINES.





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SO SEQUENCE 115 AA; 13241 MW; 745427AA3463DF71 CRC64;

Query Match 28.8%; Score 84.5; DB 1; Length 115;
Best Local Similarity 38.5%; Pred. No. 0.00068;
Matches 20; Conservative 6; Mismatches 17; Indels 9; Gaps 3;

Oy 4 CTICSDFFDHSRD-----VVAIHCGHTFHLCCLQIWFETAPSRCPGCRIOY 50
      | : | : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 44 CSIC--YNNYDEDPYLVELPHCHHKKEDELCSYWL--SRSTTCPLCRDNV 91

RESULT 25
RAPS_CHICK STANDARD; PRT; 411 AA.
AC 042393;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 43 kDa receptor-associated protein of the synapse (RAPSYN)
DE (Acetylcholine receptor-associated 43 kDa protein) (43 kDa
DE postsynaptic protein).
GN RAPSN
OS Gallus gallus (chicken).
OX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromia; Aves; Neognathae; Galiliformes; Phasianidae; Phasianinae;
ON Gallus.
RX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C;
RC MEDLINE=97331014; PubMed=9185539;
RA Burns A.L., Benson D., Howard M.J., Margiotta J.F.;
RT "Chick ciliary ganglion neurons contain transcripts coding for
RT acetylcholine receptor-associated protein at synapses (rapyn).";
RL J. Neurosci. 17:5016-5026(1997).
CC -!- FUNCTION: THOUGHT TO PLAY SOME ROLE IN ANCHORING OR STABILIZING
CC THE NICOTINIC ACETYLCHOLINE RECEPTOR AT SYNAPTIC SITES. IT MAY
CC LINK THE RECEPTOR TO THE UNDERLYING POSTSYNAPTIC CYTOSKELETON,
CC POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF POSTSYNAPTIC
CC MEMBRANES.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MUSCLE FIBERS AND IN NEURONS.
CC -!- DOMAIN: A Cysteine-rich region homologous to part of the
CC REGULATOR DOMAIN OF PROTEIN KINASE C may be important in
CC INTERACTIONS OF THIS PROTEIN WITH THE LIPID BILAYER.
CC -!- SIMILARITY: BELONGS TO THE RAPSN FAMILY.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC -----
CC EMBL: AF000138; AAB63149.1; -.
DR InterPro: IPR001237; Postsynaptic.
DR InterPro: IPR001440; TPR.
DR InterPro: IPR001841; ZnF_Ring.
DR Pfam: PF00515; TPR; 6.
DR PRINTS: PR00217; POSTSYNAPTIC.
DR ProDom: PD012428; Postsynaptic; 1.
DR SMART: SM00184; RING_1.
DR SMART: SM00028; TPR; 5.
DR PROSITE: PS00405; 43_KD_POSTSYNAPTIC; 1.
DR PROSITE: PS00518; 2F_RING_1; FALSE_NG.
DR PROSITE: PS50089; 2F_RING_2; 1.
KW Synapse; Postsynaptic membrane; Cytoskeleton; Phosphorylation;
KW Myristate; Zinc-finger.
FT INIT_MER 0 0 BY SIMILARITY.
FT ZN_FING 362 402 RING-TYPE.
```

	FT	LIPID	1	1	MYRSTATE (BY SIMILARITY).
	FT	MOD.RES	195	195	PHOSPHORYLATION (POTENTIAL).
	SQ	SEQUENCE	411 AA;	46677 MW;	851E7B2F645B459 CRC64;
		Query Match	Best Local Similarity	28.8%;	Score 84.5; DB 1; Length 411.
Oy		Matches 16;	Conservative 9;	Mismatches 15;	Indels 5; Gaps 2;
		4 CTICSDFF-DHSRDVAAIHCHTEFHLOCLIOFWFPAPRTCPPCR 47	:   :	:   :   :     :   :   :   :	
Db		362 CGMGCESTGCKNNQLPCSHFFHLKLT---	-QTNGTRGPCNCR 402		
	RESULT	26			
RNF4_HUMAN	ID	RNF4_HUMAN	STANDARD:	PRT:	190 AA.
AC		P78317:			
Dt		16-OCT-2001 (Rel. 40, Created)			
Dt		16-OCT-2001 (Rel. 40, Last sequence update)			
Dt		16-OCT-2001 (Rel. 40, Last annotation update)			
DE		RING finger protein 4.			
GN		RNF4.			
OS		Homo sapiens (Human).			
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
NX		NCBI_Taxid=9606;			
RN		[1]			
RP		SEQUENCE FROM N.A.			
RC		TISSUE-Brain:			
RA		MEDLINE:98403881; PubMed:9734812;			
RA		Hadano S., Ishida Y., Ikeda J.E.;			
RT		"The primary structure and genomic organization of five novel			
RT		transcripts located close to the Huntington's disease gene on human			
RT		chromosome 4p16.3."			
RL		DNA Res. 5:177-186(1998).			
RN		[2]			
RP		SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.			
RC		TISSUE-Brain:			
RX		MEDLINE:98140125; PubMed:9479498;			
RA		Charlotti L., Benvenuto G., Fedele M., Santoro M., Simeone A.,			
RA		Fusco A., Bruni C.B.;			
RT		"Identification and characterization of a novel RING-finger gene			
RT		(RNF4) mapping at 4p16.3;"			
RL		Genomics 47:258-265(1998).			
CC		- FUNCTION: ENHANCES STEROID RECEPTOR-MEDIATED TRANSCRIPTIONAL			
CC		ACTION AS WELL AS ACTIVATING BASAL TRANSCRIPTION (BY			
CC		SIMILARITY).			
CC		- SUBUNIT: INTERACTS WITH GSCL, ANDROGEN RECEPTOR AND TBP (BY			
CC		SIMILARITY).			
CC		- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.			
CC		- TISSUE SPECIFICITY: WIDELY EXPRESSED AT LOW LEVELS IN MANY			
CC		TISSUES; HIGHLY EXPRESSED IN TESTIS.			
CC		- SIMILARITY: CONAINS 1 RING-TYPE ZINC FINGER.			
CC		-----			
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC		use by non-profit institutions as long as its content is in no way			
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CC		entities requires a license agreement (see http://www.isb-sdb.ch/announce/			
CC		or send an email to license@isb-sdb.ch).			
CC		-----			
DR		EMBL; AB000468; BAA19122.1; .			
DR		EMBL; U95140; AAC52022.1; .			
DR		MDM; 602850; .			
DR		InterPro; IPR001841; ZnF_ring.			
DR		pfam; PF000097; zf-C3HC4_1.			
DR		SMART; SM00184; RING_1.			
DR		PROSITE; PS00518; ZF_RING_1; 1.			
DR		PROSITE; PS50089; ZF_RING_2; 1.			
KW		Transcription regulation; Activator; Zinc-finger; Nuclear protein.			
FT		ZNFING	132	177	RING-TYPE.



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DR EMBL: AF022081; AAC35248.1; -  
 DR InterPro: IPR001841; znf\_ring.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS00518; ZF\_RING\_1; 1.  
 DR PROSITE: PS50089; ZF\_RING\_2; 1.  
 KW Transcription regulation; Activator; Zinc-finger; Nuclear protein.  
 FT ZN\_FING 136 181 RING-TYPE.  
 SQ SEQUENCE 194 AA; 21896 MW; 40C13970FC1DFF2 CRC64;

Query Match 28.7%; Score 84; DB 1; Length 194;  
 Best Local Similarity 35.3%; Pred. No. 0.0013;  
 Matches 18; Conservative 7; Mismatches 20; Indels 6; Gaps 2;

QY 4 CTC-----SFFDHSRDVAAIHCGHTFHLOCLIQWETAPSRTPCPCRIQY 50  
 Db 136 CPICMGYSSEIVONGRLIVSTECGHWFCSQLRDSLKNA--NTPCPCRKRI 184

RESULT 29  
 ICP0\_HSVB7 STANDARD: PRT; 676 AA.

AC P29128;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Trans-acting transcriptional protein ICP0 (P135 protein) (IER  
 DE 2.9/ER2.6).  
 GN BICP0.  
 OS Bovine herpesvirus type 1 (strain Jura).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Varicelloviruses.  
 OX NCBI\_TaxID=31518;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=92219360; PubMed=1313901;  
 RA Wirth U V., Fraefel C., Vogt B., Vicek C., Paces V., Schwytzer M.;  
 RT "Immediate-early RNA 2.9 and early RNA 2.6 of bovine herpesvirus 1  
 RT are 3' coterminal and encode a putative zinc finger transactivator  
 RT protein.";  
 RL J. Virol. 66:2763-2772(1992).  
 CC -1- PTM: THE STRONGLY ACIDIC REGION MIGHT SERVE AS A TRANSCRIPTIONAL  
 CC ACTIVATION DOMAIN. POSSIBLY REGULATED THROUGH PHOSPHORYLATION BY  
 CC CASEIN KINASE II.

CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 CC -1- SIMILARITY: TO OTHER HERPESVIRUSES ICP0 PROTEIN.

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DR EMBL: M84465; AAA46061.1; -  
 DR EMBL: AJ004801; CAA06138.1; -  
 DR PIR: B38209; EDBE23.  
 DR HSSP: P28990; ICHC.  
 DR InterPro: IPR001841; znf\_ring.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00184; RING; 1.

DR PROSITE: PS00518; ZF\_RING\_1; 1.  
 DR PROSITE: PS50089; ZF\_RING\_2; 1.  
 DR Transcription regulation; Trans-acting factor; Activator; Zinc-finger;  
 KW

KW DNA-binding; Early protein; Repressor; Phosphorylation.  
 FT ZN\_FING 13 52 RING-TYPE.  
 FT DOMAIN 284 331 ASP/GLU-RICH (ACIDIC).  
 SQ SEQUENCE 676 AA; 67879 MW; 11B06BA4E5C4B71 CRC64;

Query Match 28.7%; Score 84; DB 1; Length 676;  
 Best Local Similarity 38.0%; Pred. No. 0.0042;  
 Matches 19; Conservative 5; Mismatches 22; Indels 4; Gaps 2;

QY 1 LSLCTICSDFFDHSRDVAAIHCGHTFHLOCLIQWETAPSRTPCPCRIQY 50  
 Db 10 LGSCCICLDIAITGA--ARALPCLHAFCLACIRRWLEGRP--TCPLCKAPV 55

RESULT 30  
 ICP0\_HSVBK STANDARD: PRT; 676 AA.

AC P29836;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Trans-acting transcriptional protein ICP0 (P135 protein) (IER  
 DE 2.9/ER2.6).  
 GN BICP0.  
 OS Bovine herpesvirus type 1 (strain K22).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Varicelloviruses.  
 OX NCBI\_TaxID=31519;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=92219360; PubMed=1313901;  
 RA Wirth U V., Fraefel C., Vogt B., Vicek C., Paces V., Schwytzer M.;  
 RT "Immediate-early RNA 2.9 and early RNA 2.6 of bovine herpesvirus 1  
 RT are 3' coterminal and encode a putative zinc finger transactivator  
 RT protein.";  
 RL J. Virol. 66:2763-2772(1992).  
 CC -1- PTM: THE STRONGLY ACIDIC REGION MIGHT SERVE AS A TRANSCRIPTIONAL  
 CC ACTIVATION DOMAIN. POSSIBLY REGULATED THROUGH PHOSPHORYLATION BY  
 CC CASEIN KINASE II.

CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 CC -1- SIMILARITY: TO OTHER HERPESVIRUSES ICP0 PROTEIN.

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DR EMBL: M84464; AAA46061.1; -  
 DR PIR: A38209; EDBE22.  
 DR HSSP: P28990; ICHC.

DR InterPro: IPR001841; znf\_ring.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS00518; ZF\_RING\_1; 1.  
 DR PROSITE: PS50089; ZF\_RING\_2; 1.  
 KW Transcription regulation; Trans-acting factor; Activator; Zinc-finger;  
 KW DNA-binding; Early protein; Repressor; Phosphorylation.  
 FT ZN\_FING 13 52 RING-TYPE.  
 FT DOMAIN 284 331 ASP/GLU-RICH (ACIDIC).  
 SQ SEQUENCE 676 AA; 67701 MW; 9BB0683CBFC6A5D CRC64;

Query Match 28.7%; Score 84; DB 1; Length 676;  
 Best Local Similarity 38.0%; Pred. No. 0.0042;  
 Matches 19; Conservative 5; Mismatches 22; Indels 4; Gaps 2;

QY 1 LSLCTICSDFFDHSRDVAAIHCGHTFHLOCLIQWETAPSRTPCPCRIQY 50  
 Db 10 LGSCCICLDIAITGA--ARALPCLHAFCLACIRRWLEGRP--TCPLCKAPV 55

RESULT 31  
 CBLB\_HUMAN STANDARD; PRT; 982 AA.  
 ID CBLB\_HUMAN 013192; 013193;  
 AC 013191; 013192; 013193;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Signal transduction protein CBL-B (SH3-binding protein CBL-B).  
 GN CBLB.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95303504; PubMed=7784085;  
 RA Keane M.M., Rivero-Lezcano O.M., Mitchell J.A., Robbins K.C.,  
 RA Lipkowitz S.;  
 RT "Cloning and characterization of cbl-b: a SH3 binding protein with  
 RT homology to the c-cbl proto-oncogene";  
 RL Oncogene 10:2367-2377(1995).  
 CC -1- SUBUNIT: INTERACTS WITH SH3 DOMAIN PROTEINS FYN, FGR AND PLCG1.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A LONG FORM (SHOWN HERE),  
 CC TRUNCATED ISOFORM 1 AND TRUNCATED ISOFORM 2; ARE PRODUCED BY  
 CC ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LUNG, KIDNEY, SPLEEN, AND TESTIS,  
 CC AS WELL AS PETAL BRAIN AND LIVER AND HEMATOPOIETIC CELL LINES, BUT  
 CC NOT IN ADULT BRAIN, LIVER, PANCREAS, SALIVARY GLAND, OR SKELETAL  
 CC MUSCLE.  
 CC -1- PTM: PHOSPHORYLATED ON TYROSINES.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 CC -1- SIMILARITY: CONTAINS 1 UBA DOMAIN.  
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 CC -----  
 DR EMBL: U26710; AAB09291.1; -  
 DR EMBL: U26711; AAB09292.1; -  
 DR EMBL: U26712; AAB09293.1; -  
 DR HSSP: P22681; 1B47.  
 DR MIM: 604491; -  
 DR InterPro: IPR003153; Cbl\_N.  
 DR InterPro: IPR000980; SH2.  
 DR InterPro: IPR000449; UBA.  
 DR InterPro: IPR001841; Znf\_ring.  
 DR Pfam: PF02262; Cbl\_N; 1.  
 DR Pfam: PF02761; Cbl\_N2; 1.  
 DR Pfam: PF02762; Cbl\_N3; 1.  
 DR Pfam: PF00627; UBA; 1.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00184; RING; 1.  
 DR SMART: SM00252; SH2; 1.  
 DR SMART: SM00165; UBA; 1.  
 DR PROSITE: PS00518; ZF\_RING\_1; 1.  
 DR PROSITE: PS50089; ZF\_RING\_2; 1.  
 KW Nuclear protein; zinc-finger; Phosphorylation; Alternative splicing.  
 FT DOMAIN 116 119 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT ZN\_FING 373 412 RING-TYPE.  
 FT DOMAIN 477 701 PRO-RICH.  
 FT DOMAIN 931 970 UBA.  
 FT VARSPPLIC 812 982 MISSING (IN TRUNCATED ISOFORM 1).  
 FT VARSPPLIC 767 770 DVED -> TVRI (IN TRUNCATED ISOFORM 2).  
 FT VARSPPLIC 771 982 MISSING (IN TRUNCATED ISOFORM 2).  
 SQ SEQUENCE 982 AA; 109479 MW; 038D4965DAFB98CB CRC64;

Query Match 28.7%; Score 84; DB 1; Length 982;  
 Best Local Similarity 35.4%; Pred. No. 0.0059;  
 Matches 17; Conservative 8; Mismatches 19; Indels 4; Gaps 2;  
 Oy 3 LCITCSDFPDHSDVAIHCGHFFHLOCLIQWFETAPSRCTPCQRIQV 50  
 Db 372 LCRICA---ENDRDVKEIEPCGHMCTSLRAMEQ-SDGQCCPCRCREI 415  
 RESULT 32  
 RAPS\_HUMAN STANDARD; PRT; 411 AA.  
 ID RAPS\_HUMAN 013702;  
 AC 013702;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 43 kDa receptor-associated protein of the synapse (RAPSIN)  
 DE (Acetylcholine receptor-associated 43 kDa protein) (43 kDa  
 DE postsynaptic protein).  
 GN RAPSIN.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Muscle;  
 RX MEDLINE=97001170; PubMed=8812503;  
 RA Buckel A., Beeson D., James M., Vincent A.;  
 RT "Cloning of cDNA encoding human rapsyn and mapping of the RAPSIN gene  
 RT locus to chromosome 11p11.2-p11.1";  
 RL Genomics 35:613-616(1996).  
 CC -1- FUNCTION: THOUGHT TO PLAY SOME ROLE IN ANCHORING OR STABILIZING  
 CC THE NICOTINIC ACETYLCHOLINE RECEPTOR AT SYNAPTIC SITES. IT MAY  
 CC LINK THE RECEPTOR TO THE UNDERLYING POSTSYNAPTIC CYTOSKELETON,  
 CC POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF POSTSYNAPTIC  
 CC MEMBRANES.  
 CC -1- DOMAIN: A CYSTEINE-RICH REGION HOMOLOGOUS TO PART OF THE  
 CC REGULATORY DOMAIN OF PROTEIN KINASE C MAY BE IMPORTANT IN  
 CC INTERACTIONS OF THIS PROTEIN WITH THE LIPID BILAYER.  
 CC -1- SIMILARITY: BELONGS TO THE RAPSIN FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 CC -----  
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 CC -----  
 DR EMBL: Z33905; CAA83954.1; -  
 DR MIM: 601592; -  
 DR InterPro: IPR001237; Postsynaptic.  
 DR InterPro: IPR001440; TPR.  
 DR InterPro: IPR001841; Znf\_ring.  
 DR Pfam: PF00515; TPR; 5.  
 DR PRINTS: PR00217; POSTSYNAPTIC.  
 DR PRODOM: PD012428; Postsynaptic; 1.  
 DR SMART: SM00184; RING; 1.  
 DR SMART: SM00028; TPR; 5.  
 DR PROSITE: PS00405; 43\_KD\_POSTSYNAPTIC; 1.  
 DR PROSITE: PS00518; ZF\_RING\_1; FALSE\_NEG.  
 DR PROSITE: PS50089; ZF\_RING\_2; 1.  
 KW Synapse; Postsynaptic membrane; Cytoskeleton; Phosphorylation;  
 FT INIT\_MET 0 0 BY SIMILARITY.  
 FT ZN\_FING 362 402 RING-TYPE.  
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).  
 FT MOD\_RES 195 195 PHOSPHORYLATION (POTENTIAL).  
 FT MOD\_RES 404 404 PHOSPHORYLATION (POTENTIAL).



SQ SEQUENCE 411 AA; 46199 MW; 6A9FBAAB95E8C6C CRC64;  
 Query Match 28.5%; Score 83.5; DB 1; Length 411;  
 Best Local Similarity 33.3%; Pred. No. 0.003;  
 Matches 15; Conservative 10; Mismatches 15; Indels 5; Gaps 2;  
 4 CTICSDFFDHSRDVAALHCGHTFHLOCLIQMFEAPSRTPCPCR 47  
 Db 362 CALCGESIGENKSRIDALPCSHIFHLKCL-----ONNGTRSCPCR 402  
 RESULT 33  
 A33\_PLEMA STANDARD; PRT; 624 AA.  
 AC 002084;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Zinc-binding protein A33.  
 OS Pleurodeles waltlilii (Iberian ribbed newt).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Caudata; Salamandridae; Salamandridae;  
 OC Pleurodeles.  
 OX NCBI\_Taxid=8319;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RA MEDLINE=93154311; PubMed=7679068;  
 RA Bellini M., Lacroix J.-C., Gall J.G.;  
 RT "A putative zinc-binding protein on lampbrush chromosome loops.";  
 RL EMO J. 12:107-114(1993).  
 CC -1- FUNCTION: MAY BE A NUCLEAR REGULATORY PROTEIN THAT IS STORED  
 IN THE GERMAL VESICLE FOR USE DURING EARLY EMBRYOGENESIS  
 AND MAY PLAY A ROLE IN THE SYNTHESIS OR PROCESSING OF PRE-MRNA  
 DURING OOGENESIS.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- DEVELOPMENTAL STAGE: IT FIRST APPEARS ON THE CHROMOSOME LOOPS  
 AND IN THE NUCLEOPLASM OF THE GERMAL VESICLE (GV). IT IS  
 TRANSMITTED TO THE EGG AT GV BREAKDOWN AND APPEARS IN EMBRYONIC  
 NUCLEI AT THE MID-BLASTULA STAGE AND IS FOUND IN MANY BUT NOT  
 ALL NUCLEI AT STILL LATER STAGES OF EMBRYOGENESIS.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 CC -1- SIMILARITY: CONTAINS 1 B BOX-TYPE ZINC FINGER.  
 CC -1- SIMILARITY: CONTAINS 1 SPRY DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL; L04190; AAA9614.1; -  
 DR InterPro: IPR003649; Bbox.C.  
 DR InterPro: IPR001870; Gamma\_carboxylase.  
 DR InterPro: IPR003877; SPRY.  
 DR InterPro: IPR003878; SPRY\_domain.  
 DR InterPro: IPR000315; znf\_bbox.  
 DR InterPro: IPR001841; znf\_fing.  
 DR Pfam; PF00662; SPRY.1.  
 DR Pfam; PF00643; zf-B\_box.1.  
 DR Pfam; PF00097; zf-C3HC4.1.  
 DR PRINTS; PR01406; BBOXZNFINGER.  
 DR SMART; SM00502; BBC.1.  
 DR SMART; SM00336; BBOX.1.  
 DR SMART; SM00184; RING.1.  
 DR SMART; SM00449; SPRY.1.  
 DR PROSITE; PS50119; ZF\_BBOX.1.  
 DR PROSITE; PS00518; ZF\_RING.1.  
 DR PROSITE; PS50089; ZF\_RING\_2; 1.  
 KW Zinc-finger; Nuclear protein; Developmental protein; Coiled coil;

KW RNA-binding. 19 26  
 FT DOMAIN 134 149 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT ZN\_FING 162 202 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT ZN\_FING 238 269 RING-TYPE.  
 FT DOMAIN 337 386 B BOX-TYPE.  
 FT DOMAIN 449 619 COILED COIL.  
 FT SPRY 619  
 SQ SEQUENCE 624 AA; 71056 MW; 60DBD1F3F071EFED CRC64;  
 Query Match 28.5%; Score 83.5; DB 1; Length 624;  
 Best Local Similarity 29.5%; Pred. No. 0.0044;  
 Matches 13; Conservative 12; Mismatches 16; Indels 3; Gaps 1;  
 4 CTICSDFFDHSRDVAALHCGHTFHLOCLIQMFEAPSRTPCPCR 47  
 Db 162 CPLCRSLF---KEPVILECGHNFCKHCIDKSWESASAFSCPECK 202  
 RESULT 34  
 RNF6\_HUMAN STANDARD; PRT; 685 AA.  
 ID RNF6\_HUMAN  
 AC Q9Y252; Q9UP41;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE RING finger protein 6.  
 GN RNF6.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Leukocyte;  
 RA MEDLINE=99265977; PubMed=10331950;  
 RA McDonald D.H.C., Lahiri D., Sampath A., Chase A., Sohal J.,  
 RA Cross N.C.P.;  
 RT "Cloning and characterization of RNF6, a novel RING finger gene  
 mapping to 13q12.";  
 RL Genomics 58:94-97(1999).  
 RN [2]  
 RP SEQUENCE OF 320-685 FROM N.A.  
 RC TISSUE=Testis;  
 RA Blum H., Bauersachs S., Mewes H.-W., Gassenhuber J., Wiemann S.;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- TISSUE SPECIFICITY: WEAKLY EXPRESSED IN PERIPHERAL BLOOD, SPLEEN,  
 PROSTATE, TESTIS AND OVARY.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 CC -----  
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 CC -----  
 DR EMBL; AJ010347; CAB40414.1; -  
 DR EMBL; AJ010346; CAB40413.1; -  
 DR EMBL; AL133621; CAB63747.1; -  
 DR HSSP; P28990; ICHC.  
 DR MTR; 604242; -  
 DR InterPro: IPR001841; znf\_fing.  
 DR Pfam; PF00097; zf-C3HC4.1.  
 DR SMART; SM00184; RING.1.  
 DR PROSITE; PS00518; ZF\_RING.1; FALSE\_NEG.  
 DR PROSITE; PS50089; ZF\_RING\_2; 1.  
 KW Zinc-finger.  
 FT DOMAIN 292 424 ARG-RICH.  
 FT DOMAIN 598 601 POLY-ASP.  
 FT ZN\_FING 632 673 RING-TYPE.  
 SQ SEQUENCE 685 AA; 78091 MW; 344584773F2E5ERC CRC64;



DR SMART; SM00028; TPR; 3.  
DR PROSITE; PS00405; 43\_KD\_POSTSYNAPTIC; 1.  
DR PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
DR PROSITE; PS50089; ZF\_RING\_2; 1.  
KW Synapse; Postsynaptic membrane; Cytoskeleton; Phosphorylation;  
MYristate; Zinc-finger.  
FT INIT\_MET 0  
FT ZN\_RING 362 402 RING-TYPE.  
FT LIPID 1 1 MYRISTATE.  
FT MOD\_RES 195 195 PHOSPHORYLATION (POTENTIAL).  
FT MOD\_RES 404 404 PHOSPHORYLATION (POTENTIAL).  
FT CONFLICT 343 344 DV -> EL (IN REF. 2).  
SQ SEQUENCE 411 AA; 46233 MW; 1085A5C709FD1E56 CRC64;

Query Match 28.2%; Score 82.5; DB 1; Length 411;  
Best Local Similarity 33.3%; Pred. No. 0.004;  
Matches 15; Conservative 10; Mismatches 15; Indels 5; Gaps 2;

QY 4 CTICSDFF-DHSRDVAIHGCHTHLQCLIQWETAPSRTPCPCR 47  
ID 362 CGCGESIGERNRLQALPCSHIFHLRCL-----QNGNTRSCPNCR 402

RESULT 37  
ID YUES\_CAEEL STANDARD; PRT; 564 AA.  
AC P90859; P90852;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical 64.7 kDa protein F26E4.11 in chromosome 1.  
GN F26E4.11.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
OC Rhabditidae; Peloderae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPRAIN-BRISTOL NZ;  
RA Lightning J., Baynes C.;  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
CC  
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CC  
CC EMBL; Z81070; CAB03009.1; -  
DR EMBL; Z81075; CAB03009.1; JOINED.  
DR EMBL; Z81075; CAB03049.1; -  
DR EMBL; Z81070; CAB03049.1; JOINED.  
DR WormPep; F26E4.11; CE096955.  
DR InterPro; IPR003892; CUE.  
DR InterPro; IPR001841; Znf\_ring.  
DR Pfam; PF02845; CUE; 1.  
DR Pfam; PF00097; zf-C3HC4; 1.  
DR SMART; SM00546; CUE; 1.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
DR PROSITE; PS50089; ZF\_RING\_2; 1.  
KW Hypothetical protein; Zinc-finger.  
FT ZN\_RING 335 373 RING-TYPE.  
SQ SEQUENCE 564 AA; 64709 MW; 7C790C238207E49B CRC64;

Query Match 28.2%; Score 82.5; DB 1; Length 564;  
Best Local Similarity 34.0%; Pred. No. 0.0054;  
Matches 16; Conservative 6; Mismatches 20; Indels 5; Gaps 2;

QY 4 CTICSDFFDHSRDVAIHGCHTHLQCLIQWETAPSRTPCPCR 50  
ID 335 CVVCEWELGSR---RLPCSHQHDWCLMWWL--ADSSCPICRCRI 376

RESULT 38  
ID MKRL\_MACEU STANDARD; PRT; 478 AA.  
AC Q9T91;  
DT 01-MAR-2002 (Rel. 41, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Makorin 1.  
GN MKRN1.  
OS Macropus eugenii (Tanner wallaby).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.  
OX NCBI\_TaxID=9315;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-20304755; PubMed-10843807;  
RA Gray T.A., Hernandez L., Carey A.H., Schladach M.A., Smithwick M.J.,  
RA Rus K., Marshall Graves J.A., Stewart C.L., Nicholls R.D.;  
RT "The ancient source of a distinct gene family encoding proteins  
RT featuring RING and C(3)H zinc-finger motifs with abundant expression  
RT in developing brain and nervous system."  
RL Genomics 66:76-86(2000).  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
CC -1- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.  
CC  
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CC  
CC EMBL; AF192786; AAP17489.1; -  
DR InterPro; IPR001395; Aldo\_ket\_red.  
DR InterPro; IPR000571; Zf-CCCH.  
DR InterPro; IPR001841; Znf\_ring.  
DR Pfam; PF00097; zf-C3HC4; 1.  
DR Pfam; PF00642; zf-CCCH; 4.  
DR SMART; SM00356; Znf\_C3H1; 4.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS00518; ZF\_RING\_1; 4.  
DR PROSITE; PS50089; ZF\_RING\_2; 1.  
KW Zinc-finger; Repeat.  
FT ZN\_RING 57 75 C3H1-TYPE 1.  
FT ZN\_RING 86 104 C3H1-TYPE 2.  
FT ZN\_RING 210 228 C3H1-TYPE 3.  
FT DOMAIN 232 259 MAKORIN-TYPE CYS-HIS.  
FT ZN\_RING 277 331 C3H1-TYPE 4.  
FT ZN\_RING 366 386 C3H1-TYPE 4.  
SQ SEQUENCE 478 AA; 52905 MW; CB2D9B147433853E CRC64;

Query Match 27.8%; Score 81.5; DB 1; Length 478;  
Best Local Similarity 29.8%; Pred. No. 0.0061;  
Matches 17; Conservative 11; Mismatches 18; Indels 11; Gaps 2;

QY 3 LCTICSDFF-----DHSRDVAIHGCHTHLQCLIQWETAPSRTPCPCR 48  
ID 276 VCGICMEVVEKAPNSERRFGILNCNHTYCLCKIRKMSAKOFESKIIKSCPCERI 332

RESULT 39  
ID MKRL\_MOUSE STANDARD; PRT; 481 AA.  
AC Q9QXP6;  
DT 01-MAR-2002 (Rel. 41, Created)

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DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DT Makorin 1.
GN MKRNL
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20304755; PubMed-10843807;
RA Gray T.A., Hernandez L., Carey A.H., Schaldach M.A., Smithwick M.J.,
RA Rus K., Marshall Graves J.A., Stewart C.L., Nicholls R.D.;
RT "The ancient source of a distinct gene family encoding proteins
RT featuring RING and C(3)H zinc-finger motifs with abundant expression
RT in developing brain and nervous system.";
RL Genomics 66:76-86(2000).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF192785; AAF17488.1; -
DR MGD; MGI:1859353; Mkrnl.
DR InterPro: IPR000571; Zf-CCCH.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; Zf-CCCH4; 1.
DR Pfam: PF00642; Zf-CCCH4; 4.
DR SMART: SM00184; RING; 1.
DR SMART: SM00356; Znf_C3H1; 4.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Zinc-finger; Repeat.
KW ZN_FING 61 79 C3H1-TYPE 1.
FT ZN_FING 90 108 C3H1-TYPE 2.
FT ZN_FING 214 232 C3H1-TYPE 3.
FT DOMAIN 236 263 MAKORIN-TYPE CYS-HIS.
FT ZN_FING 281 335 RING-TYPE.
FT ZN_FING 370 390 C3H1-TYPE 4.
FT ZN_FING 481 AA; 53008 MW; B6BDE5E785CEAE CRC64;
SQ SEQUENCE

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Query Match 27.8%; Score 81.5; DB 1; Length 481;
Best local Similarity 29.8%; Pred. No. 0.0062;
Matches 17; Conservative 11; Mismatches 18; Indels 11; Gaps 2;
OY 3 LCITCSDFF-----DHSRDVAIHCGHTFLDCLLIOW-----FETAPSRCTPCPCR 48
DB 280 VCGICMEVYEKANPSERRRFGILSNCHNYCLCKIRKWSAKOFESKIIKSCPCR 336

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RESULT 40
MKRL_HUMAN STANDARD; PRT; 482 AA.
AC Q9UHC7; Q9UEZ7; Q9H0G0;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Makorin 1.
GN MKRNL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20304755; PubMed-10843807;

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```

RA Gray T.A., Hernandez L., Carey A.H., Schaldach M.A., Smithwick M.J.,
RA Rus K., Marshall Graves J.A., Stewart C.L., Nicholls R.D.;
RT "The ancient source of a distinct gene family encoding proteins
RT featuring RING and C(3)H zinc-finger motifs with abundant expression
RT in developing brain and nervous system.";
RL Genomics 66:76-86(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-21154917; PubMed-11230166;
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Ansoerge W., Boecker M., Bloecker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA Mewes H.-W., Oltmannseder B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Poustka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs.";
RL Genome Res. 11:422-435(2001).
CC -1- TISSUE SPECIFICITY: Ubiquitous.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
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CC -----
DR EMBL: AF192784; AAF17487.1; -
DR EMBL: AF192793; AAF18979.1; -
DR EMBL: AF192789; AAF18979.1; JOINED.
DR EMBL: AF192790; AAF18979.1; JOINED.
DR EMBL: AF192791; AAF18979.1; JOINED.
DR EMBL: AF192792; AAF18979.1; JOINED.
DR EMBL: AF192792; AAF18979.1; JOINED.
DR EMBL: AL136812; CAB6746.1; -
DR InterPro: IPR000571; Zf-CCCH.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; Zf-CCCH4; 1.
DR Pfam: PF00642; Zf-CCCH4; 4.
DR SMART: SM00184; RING; 1.
DR SMART: SM00356; Znf_C3H1; 4.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Zinc-finger; Repeat; Polymorphism.
KW ZN_FING 61 79 C3H1-TYPE 1.
FT ZN_FING 90 108 C3H1-TYPE 2.
FT ZN_FING 214 232 C3H1-TYPE 3.
FT DOMAIN 236 263 MAKORIN-TYPE CYS-HIS.
FT ZN_FING 281 335 RING-TYPE.
FT ZN_FING 370 390 C3H1-TYPE 4.
FT ZN_FING 482 AA; 53363 MW; C993DECD131691C CRC64;
SQ SEQUENCE

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Query Match 27.8%; Score 81.5; DB 1; Length 482;
Best local Similarity 29.8%; Pred. No. 0.0062;
Matches 17; Conservative 11; Mismatches 18; Indels 11; Gaps 2;
OY 3 LCITCSDFF-----DHSRDVAIHCGHTFLDCLLIOW-----FETAPSRCTPCPCR 48
DB 280 VCGICMEVYEKANPSERRRFGILSNCHNYCLCKIRKWSAKOFESKIIKSCPCR 336

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Job time: 501 sec

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